

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga  
Hawkins, Phillip R.  
Hillman, Jennifer L.  
Lal, Preeti  
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN SERINE  
CARBOXYPEPTIDASE
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0241 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) IMMEDIATE SOURCE:
  - (A) LIBRARY: MPMONOT13
  - (B) CLONE: 442014

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5					10					15	
Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
	50					55					60				
Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Asp	Phe	Leu	Thr	Val
65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85				90						95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Glu	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
			115				120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165				170						175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215						220			
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275					280						285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys
	355					360						365			
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn
	370					375					380				
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu
385					390					395					400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Gln	Tyr	Lys	Lys	Ala	Glu	Lys
				405					410					415	
Lys	Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Gly	Val	Ala	Gly	Tyr
			420					425					430		
Ile	Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly
	435					440						445			
His	Thr	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn

450                                      455                                      460  
 Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465                                      470                                      475

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MPHENOT03  
 (B) CLONE: 443004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AAGCGCTGCA AGGACAACCG GCTGGGGTCC TTGGGGGGGG GGCTCAGGGA CCAGCACCGA      60
CTGCGCCGCA CCTGAGAGA TGGTTGGTGC CATGTGGAAG GTGATTGTTT CGCTGGTCC      120
GTTGATGCCT GGGCCCTGTG ATGGGCTGTT TCACTCCCTA TACAGAAGTG TTTCCATGCC      180
ACCTAAGGGA GACTCAGGAC AGCCATTATT TCTCACCCCT TACATTGAAG CTGGGAAGAT      240
CCAAAAAGGA AGAGAATTGA GTTTGGTGGG TCCTTTCCCA GGAAGAGTA TGAAGAGTTA      300
TGCCGACTTC CTCACTGTGA ATAAGACTTA CAACAGCAAC CTCTCTTCTT GGTTCCTTCC      360
AGCTCAGATA CAGCCAGAAG ATGCCCCAGT AGTTCTCTGG CTACAGGGTG AGCCGGGAGG      420
TTCATCCATG TTTGGACTCT TTGTGGAACA TGGGCCCTTAT GTTGTCAACA GTAACATGAC      480
CTTGCGTGAC AGAGACTTCC CCTGGACCAC AACGCTCTCC ATGCTTTACA TTGACAATCC      540
AGTGGGCACA GGCTTCAGTT TTACTGATGA TACCCACGGA TATGCAGTCA ATGAGGACGA      600
TGTAGCACGG GATTTATACA GTGCACTAAT TCAGTTTTTC CAGATATTTT CTGAATATAA      660
AAATAATGAC TTTTATGTCA CTGGGGAGTC TTATGCAGGG AAATATGTGC CAGCCATTGC      720
ACACCTCATC CATTCCTCCA ACCCTGTGAG AGAGGTGAAG ATCAACCTGA ACCGAATTGC      780
TATTGGAGAT GGATATTTCTG ATCCCGAATC AATTATAGGG GGCTATGCAG AATTCCTGTA      840
CCAAATTTGGC TTGTTTGGATG AGAAGCAAAA AAAGTACTTC CAGAAGCAGT GCCATGAATG      900
CATAGAACAC ATCAGGAAGC AGAACTGGTT TGAGGCCCTT GAAATACTGG ATAACTACT      960
AGATGGCGAC TTAACAAGTG ATCCTTCTTA CTTCAGAAAT GTTACAGGAT GTAGTAATTA     1020
CTATAACTTT TTGCGGTGCA CGSAACCTGA GGATCAGCTT TACTATGTGA AATTTTTGTC     1080
ACTCCACAGG GTGAGACAAG CCATCCACGT GGGGAATCAG ACTTTTAATG ATGGAACTAT     1140
AGTTGAAAAG TACTTGGGAG AAGATACAGT ACAGTCAGTT AAGCCATGGT TAACTGAAAT     1200
CATGAATAAT TATAAGGTTT TGATCTACAA TGGCCAACTG GACATCATCG TGGCAGCTGC     1260
CCTGACAGAG CGCTCCTTGA TGGGCATGGA CTGGAAAAGG TCCCAGGAAT ACAAGAAGGC     1320
AGAAAAAAAA AAAGTTTGGG AGATCTTTAA ATCTGACAGT GGAGTGGCTG GTTACATCCG     1380
GCAAGTGGGT GACTTCCATC AGGTAATTAT TCGAGGTGGA GGACATACTT TACCCTATGA     1440
CCAGCCTCTG AGAGCTTTTG ACATGATTAA TCGATTCAAT TATGGAAAAG GATGGGATCC     1500
TTATGTTGGA TAACTTACCT TCCAAAAGA GAACATCAGA GGTTTTCAAT GCTGAAAAGA     1560
AAATCGTAAA AACAGAAAAT CTCTATAGGA TAAAAAATT ATCTTTTCAT ATCTGCAAGA     1620
TCTTTTTCAT CAATAAAAAT TATCCTTGAA ACAAAAAAAA AAAGAAAAAG     1670

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT11  
 (B) CLONE: 566993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5					10					15	
Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
	50					55					60				
Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85				90						95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Xaa	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
			115				120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Xaa	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165				170						175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275					280						285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
			325						330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys
	355						360					365			
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn
	370					375					380				
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu
385					390					395					400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys	Ala	Glu	Lys
			405						410					415	
Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala	Gly	Tyr	Ile
	420							425					430		
Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly	His
	435					440						445			
Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn	Arg

450                                      455                                      460  
 Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465                                      470                                      475

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01  
 (B) CLONE: 564993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

GAAAGCTGGT ACGCCTGCNG GTNCCGGTCC GGAATTGCGG GGTNGACCCA CGCCTCCGAN      60
CGACTGCGCC GCACCCCTGAG AGATGGTTGG TGCCATGTGG AAGGTGATTG TTTGCTGGT      120
CCTGTTGATG CCTGCCCCCT GTGATGGGCT GTTTCACCTC CTATACAGAA GTGTTTCCAT      180
GCCACCTAAG GGAGACTCAG GACAGCCATT ATTTCTCACC CCTTACATTG AAGCTGGGAA      240
GATCCAAAAA GGAAAGAGAA TGAGTTTGGT CGGCCCTTTC CCAGGACTGA ACATGAAGAG      300
TTATGCCGGC TTCTTCACCG TGAATAAGAC TTACAACAGC AACCTCTTCT TCTGGTTCTT      360
CCCAGCTCAG ATACAGCCAG AAGATGCCCC AGTAGTTCTC TGGCTACAGG GTGGGCCGGG      420
AGGTTTCATC ATGTTWGGAC TCTTTGTGGA ACATGGGCTC TATGTTGTCA CAAGTAACAT      480
GACCTTGGCT GACAGAGACT TCCCCTGGAC CACAACGCTC TCCATGCTTT ACATTGACAA      540
TCCAGTGGGC ACAGGCTTCA GTTTTACTGA TGATACCCAC GGATATGCAG TCAATGAGGA      600
CGATGTAGCA CGGATTTTAT ACAGTGCCTT AATTCAGTTT TTCCAGATAT TTCTGAATA      660
TAAAAATAAT GACTTTTATG TCACTGGGGA GTCTTATGCA GGGAAATATG TGCCAGCCAT      720
TGCACACCTC ATCCATTCCC TCAACCTGTG GAGAGAGCTG AAGATCAACC TGAACGGAAT      780
TGCTATTGGA GATGGATATT CTGATCCCGA ATCAATTATA GGGGGCTATG CAGAATTCCCT      840
GTACCAAATT GCCTGTGTTG ATGAGAAGCA AAAAAAGTAC TTCCAGAAGC AGTGCCATGA      900
ATGCATAGAA CACATCAGGA AGCAGAACTG GTTTGAGGCC TTTGAAATAC TGGATAAACT      960
ACTAGATGGC GACTTAACAA GTGATCCTTC TTACTTCCAG AATGTTACAG GATGTAGTAA     1020
TTACTATAAC TTTTTCGGGT GCACGGAACC TGAGSATCAG CTTTACTATG TGAAATTTTT     1080
GTCACTCCCA GAGTTCAGAC AAGCCATCCA CGTGGGGAAT CAGACTTTTA ATGATGGAAC     1140
TATAGTTGAA AAGTACTTGC GAGAAGATAC AGTACAGTCA GTTAAGCCAT GGTTAACATG     1200
AATCATGAAT AATTATAAGG TTCTGATCTA CAATGGCCAA CTGGACATCA TCGTGGCAGC     1260
TGCCCTGACA GAGGCTCCTT TGATGGGCTT GGAATGGAAA GGTTCGCCAGG AATACAAGAA     1320
GGCAGAAAAA AAAGTTTGGG AGATCTTTAA ATCTGACAGT GAAGTGGCTG GTTACATCCG     1380
GCAAGTGGGT GACTTTCATC AGGTAAATTAT TCGAGGTGGA GGACATATTT TACCCATATG     1440
CCAGCCTCTG AGAGCTTTTG ACATGATTAA TCGATTCAAT TATGGAAAAG GATGGGATCC     1500
TTATGTTGGA TAACTACCT TCCAAAAAGA GAACATCAGA GGTTTTCATN T      1561

```

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCT01  
 (B) CLONE: TUP469

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5				10					15		
Pro	Gly	Pro	Cys	Gly	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Tyr	Thr	Gly	Thr	Asn	Ser	Val	Phe	Gln	Ile
	50				55					60					
Phe	Pro	Glu	Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr
65				70					75					80	
Ala	Gly	Lys	Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn
				85				90						95	
Pro	Val	Arg	Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp
			100					105					110		
Gly	Tyr	Ser	Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu
	115						120					125			
Tyr	Gln	Ile	Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys
	130					135					140				
Gln	Cys	His	Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu
145					150					155				160	
Ala	Phe	Glu	Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp
				165					170					175	
Pro	Ser	Tyr	Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe
			180					185						190	
Leu	Arg	Cys	Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu
	195					200						205			
Ser	Leu	Pro	Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe
	210					215					220				
Asn	Asp	Gly	Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln
225					230					235				240	
Ser	Val	Lys	Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu
			245					250						255	
Ile	Tyr	Asn	Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu
	260						265						270		
Arg	Ser	Leu	Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys
	275					280						285			
Ala	Glu	Lys	Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala
	290					295					300				
Gly	Tyr	Ile	Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly
305				310					315					320	
Gly	Gly	His	Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met
			325					330						335	
Ile	Asn	Arg	Phe	Ile	Tyr	Gly	Lys	Gly	Trp	Asp	Pro	Tyr	Val	Gly	
			340					345					350		

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRT01
- (B) CLONE: 770469

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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AAGGCAAAACC GGTGCGGGTC CTTGGCGGCGC GGGGCTCAGG GAGGAGCACC GAATGCCCCG      50
CACCGTGAAGA GATGGTTGGT GCCAGTGGGA AGGTGATTGT TTGGCTGGTC CTGTTGATGC      100
CTGGCCCCCGT TGGTGGGCTG TTCTACTGCC TATACAGAAG TGTTTCCATG CCACCPAAGG      150
GAGACTCAGG ACAGCCATTA TTCTCAGCC CTTACATTGA AGCTGGGAAG ATTTATACAG      200
GCCTAATTC AGTTTCCAG ATATTTCCCG AATATAAAAA TAATGACITT TATGTCACTG      250
GGGAGTCCTTA TGCAGGGAAA TATGTGCCAG CCATTGCGACA CCGCATCCAT TCCCTCAAGC      300
CTGTGAGAGA GGTGAAGATC AACCCTGAACG GAATTGCTAT TGGAGATGGA TATCTGATC      350
CCGAATCAAT TATAGGGGGC TATGCGAAT TCCCTGACCA AATTGGCTTG TTGGATGAGA      400
AGCAAAAAAA GACTTTCCAG AAGCAGTGCC ATGAATGCAT AGAACACATC AGGAAGCAGA      450
ACTGGTTTGA GGCCTTTGAA ATACTGGATA AACTACTAGA TGGCGACTTA ACAAGTGATC      500
CTTCTTACTT CCAGAAATGT ACAGGATGTA GTAATTACTA TAACTTTTTG CCGTGCACTG      550
AACCTGAGGA TCAGCTTTAC TATGTGAAAT TTTTGTCACT CCCAGAGGTG AGACAAGCCA      600
TCCAGCTGGG GAATCAGACT TTTAATGATG GAATATAGT TGAAAAGTAC TGGGAGAAG      650
ATACAGTACA GTCAGTTAAG CCATGTTAA CTGAAATCAT GAATAATTAT AAGGTTCTGA      700
TCTACAATGG CCAACTGGAC ATCATCGTGG CAGCTGCCCT GACAGAGCGC TCCTTGATGG      750
GCATGGACTG GAAAGGATCC CAGGAATACA AGAAGGCAGA AAAAAAAGTT TGGGAAGATCT      800
TTAAATCTGA CAGTGAAGTG GCTGGTTACA TCCCGCAAGT GGGTGAAGTC CATCAGGTAA      850
TTATTCGAGG TGGAGGACAT ATTTTACCC ATGACCAGCC TCTGAGAGCT TTTGACATGA      900
TTAATCGATT CATTTATGGA AAAGGATGGG ATCTTATGT TGGATAAAGT ACCTTCCCAA      950
AAGAGAACAT CAGAGGTTTT CATTGCTGAA AAGAAAATCG TAAAAACAGA AAATGTCATA      1000
GGAATAAAAA AATTATCTTT TCATATCTGC AAGATTTTTT TCATCAATAA AAATTATCCT      1050
TGA

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## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1713107

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Val Lys Phe His Leu Leu Val Leu Ile Ala Phe Thr Cys Tyr Thr
 1             5             10             15
Cys Ser Asp Ala Thr Leu Trp Asn Pro Tyr Lys Lys Leu Met Arg Gly
 20             25             30
Ser Ala Ser Pro Pro Arg Pro Gly Glu Ser Gly Glu Pro Leu Phe Leu
 35             40             45
Thr Pro Leu Leu Gln Asp Gly Lys Ile Glu Glu Ala Arg Asn Lys Ala
 50             55             60
Arg Val Asn His Pro Met Leu Ser Ser Val Glu Ser Tyr Ser Gly Phe
 65             70             75             80
Met Thr Val Asp Ala Lys His Asn Ser Asn Leu Phe Phe Trp Tyr Val
 85             90             95
Pro Ala Lys Asn Asn Arg Glu Gln Ala Pro Ile Leu Val Trp Leu Gln
100             105             110
Gly Gly Pro Gly Ala Ser Ser Leu Phe Gly Met Phe Glu Glu Asn Gly
115             120             125
Pro Phe His Ile His Arg Asn Lys Ser Val Lys Gln Arg Glu Tyr Ser
130             135             140
Trp His Gln Asn His His Met Ile Tyr Ile Asp Asn Pro Val Gly Thr
145             150             155             160
Gly Phe Ser Phe Thr Asp Ser Asp Glu Gly Tyr Ser Thr Asn Glu Glu
165             170             175

```

```

His Val Gly Glu Asn Leu Met Lys Phe Ile Gln Gln Phe Phe Val Leu
180 185 190
Phe Pro Asn Leu Leu Lys His Pro Phe Tyr Ile Ser Gly Glu Ser Tyr
195 200 205
Gly Gly Lys Phe Val Pro Ala Phe Gly Tyr Ala Ile His Asn Ser Gln
210 215 220
Ser Gln Pro Lys Ile Asn Leu Gln Gly Leu Ala Ile Gly Asp Gly Tyr
225 230 235 240
Thr Asp Pro Leu Asn Gln Leu Asn Tyr Gly Glu Tyr Leu Tyr Glu Leu
245 250 255
Gly Leu Ile Asp Leu Asn Gly Arg Lys Lys Phe Asp Glu Asp Thr Ala
260 265 270
Ala Ala Ile Ala Cys Ala Glu Arg Lys Asp Met Asn Ser Ala Asn Arg
275 280 285
Leu Ile Gln Gly Leu Phe Asp Gly Leu Asp Gly Gln Glu Ser Tyr Phe
290 295 300
Lys Lys Val Thr Gly Phe Ser Ser Tyr Tyr Asn Phe Ile Lys Gly Asp
305 310 315 320
Glu Glu Ser Lys Gln Asp Ser Val Leu Met Glu Phe Leu Ser Asn Pro
325 330 335
Glu Val Arg Lys Gly Ile His Val Gly Glu Leu Pro Phe His Asp Ser
340 345 350
Asp Gly His Asn Lys Val Ala Glu Met Leu Ser Glu Asp Thr Leu Asp
355 360 365
Thr Val Ala Pro Trp Val Ser Lys Leu Leu Ser His Tyr Arg Val Leu
370 375 380
Phe Tyr Asn Gly Gln Leu Asp Ile Ile Cys Ala Tyr Pro Met Thr Val
385 390 395 400
Asp Phe Leu Met Lys Met Pro Phe Asp Gly Asp Ser Glu Tyr Lys Arg
405 410 415
Ala Asn Arg Glu Ile Tyr Arg Val Asp Gly Glu Ile Ala Gly Tyr Lys
420 425 430
Lys Arg Ala Gly Arg Leu Gln Glu Val Leu Ile Arg Asn Ala Gly His
435 440 445
Met Val Pro Arg Asp Gln Pro Lys Trp Ala Phe Asp Met Ile Thr Ser
450 455 460
Phe Thr His Lys Asn Tyr Leu
465 470

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 190283

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln
20 25 30
Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg
35 40 45

```



Gln Tyr Ser Gly Tyr Leu Lys Ser Ser Gly Ser Lys His Leu His Tyr																	
50						55					60						
Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val Val Leu						70					75						80
55																	
Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Thr						85					90						95
Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu Glu Tyr						100					105						110
Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu Glu Ser						115					120						125
Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala Thr						125					130						
Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp Phe						135					140						
145						150					155						160
Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr Gly						165					170						175
Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val Met						180					185						190
Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly Leu						195					200						205
Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr Tyr						210					215						220
His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His Cys						225					230						235
Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu Cys						240					245						250
Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly Leu						255					260						265
Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser His						270					275						280
Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn Ile						285					290						295
Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu Arg						300					305						310
Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala						315					320						325
Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile						330					335						340
Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu						345					350						355
Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu						360					365						370
Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp						375					380						385
Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn						390					395						400
Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp						405					410						415
Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile Ala						420					425						430
Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys Pro						435					440						445
Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro Tyr						450					455						460
465						470					475						480